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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	785.5	37.3	220	14	Q9JH84	Q9Jh84 unclassified
2	784.5	37.3	219	14	Q9JH92	Q9Jh92 unclassified
3	783.5	37.2	219	14	Q9JH91	Q9Jh91 unclassified
4	780.5	37.1	219	14	Q9JH89	Q9Jh89 unclassified
5	779.5	37.0	219	14	Q9JH87	Q9Jh87 unclassified
6	772.5	36.7	219	14	Q9JH90	Q9Jh90 unclassified
7	769.5	36.5	217	14	Q9JH95	Q9Jh95 unclassified
8	766.5	36.4	220	14	Q9JH83	Q9Jh83 unclassified
9	764.5	36.3	219	14	Q9JH86	Q9Jh86 unclassified
10	762.5	36.2	221	14	Q9JH94	Q9Jh94 unclassified
11	759.5	36.1	219	14	Q9JH88	Q9Jh88 unclassified
12	755.5	35.9	220	14	Q9JH93	Q9Jh93 unclassified
13	750.5	35.6	220	14	Q9JH85	Q9Jh85 unclassified
14	745.5	35.4	220	14	Q9JH96	Q9Jh96 unclassified
15	718.34	33.1	305	3	Q93782	Q93782 humicola gr
16	705.5	33.5	410	3	Q9P868	Q9P868 pirotyomece

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QY 363 DNPTMTFKEVTCPAELTTRSGCER 386
Db 196 DNPSINFNQVTCPSLTIARTNCKR 219

RESULT 2
QYH92          PRELIMINARY;      PRT;      219 AA.
AC QYH92;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TremBLrel. 20, Last annotation update)
DE Family 45 cellulase homologue.
OS unclassified eukaryotes.
OC Eukaryota.
OX NCBI_TaxID=42452;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
RL protists in the hindgut of termite Reticulitermes speratus.";
DR EMBL; AB045171; BAA98041.1; -
DR HSSP; P43316; 2ENG.
DR InterPro; IPR000334; GH_45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.
SQ SEQUENCE 219 AA; 23001 MW; 5F2EB81A6DE926CE CRC64;

Query Match      37.3%; Score 784.5; DB 14; Length 219;
Best Local Similarity 66.2%; Pred. No. 1.1e-42;
Matches 135; Conservative 29; Mismatches 37; Indels 3; Gaps 2;

QY 185 SGSTRYWDCCKASCWPVKASVTGPVDTCASNGISLLDAN--AOSGCGNGGFMCMNNQ 242
Db 16 SGRTRYWDCCKASCWEKAAVTQPVDTCKGQTRVASNDTVKSCDGGEGYCYDQA 75

QY 243 PAVNDELAYGFAAASAGNEAGWCCGCGCYELTFTSGAASGKKMVMVQVNTTGGDLGSHF 302
Db 76 PAVNDSVAYGFAAAACCG-GESGACCCYELTFTSGVPNGKMMVQVNTTGGDLGSHF 134

QY 303 DLOMPGGVGIFNGCAAGWAPNDGARGYGVSSVSDCASLPSALQAGCKWRNWFKN 362
Db 135 DLAIPEGVGVIYNGCTQSGAPADGWGSRYSRSECSQLPSGLQAGCQWRFDWFQNA 194

QY 363 DNPTMTFKEVTCPAELTTRSGCER 386
Db 196 DNPSINFNQVTCPSLTIARTNCKR 219

RESULT 3
QYH91          PRELIMINARY;      PRT;      219 AA.
AC QYH91;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TremBLrel. 20, Last annotation update)
DE Family 45 cellulase homologue.
OS unclassified eukaryotes.
OC Eukaryota.
OX NCBI_TaxID=42452;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
RL protists in the hindgut of termite Reticulitermes speratus.";
DR EMBL; AB045172; BAA98042.1; -
DR HSSP; P43316; 2ENG.
DR InterPro; IPR000334; GH_45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.

QY 363 DNPTMTFKEVTCPAELTTRSGCER 386
Db 196 DNPSINFNQVTCPSLTIARTNCKR 219

Query Match      37.3%; Score 784.5; DB 14; Length 219;
Best Local Similarity 66.2%; Pred. No. 1.1e-42;
Matches 135; Conservative 29; Mismatches 37; Indels 3; Gaps 2;

QY 185 SGSTRYWDCCKASCWPVKASVTGPVDTCASNGISLLDAN--AOSGCGNGGFMCMNNQ 242
Db 16 SGRTRYWDCCKASCWEKAAVTQPVDTCKGQTRVASNDTVKSCDGGEGYCYDQA 75

QY 243 PAVNDELAYGFAAASAGNEAGWCCGCGCYELTFTSGAASGKKMVMVQVNTTGGDLGSHF 302
Db 76 PAVNDSVAYGFAAAACCG-GESGACCCYELTFTSGVPNGKMMVQVNTTGGDLGSHF 134

QY 303 DLOMPGGVGIFNGCAAGWAPNDGARGYGVSSVSDCASLPSALQAGCKWRNWFKN 362
Db 135 DLAIPEGVGVIYNGCTQSGAPADGWGSRYSRSECSQLPSGLQAGCQWRFDWFQNA 194

QY 363 DNPTMTFKEVTCPAELTTRSGCER 386
Db 196 DNPSINFNQVTCPSLTIARTNCKR 219

Query Match      37.1%; Score 780.5; DB 14; Length 219;
Best Local Similarity 64.2%; Pred. No. 1.9e-42;
Matches 131; Conservative 33; Mismatches 37; Indels 3; Gaps 2;

QY 185 SGSTRYWDCCKASCWPVKASVTGPVDTCASNGISLLDAN--AOSGCGNGGFMCMNNQ 242
Db 16 SGRTRYWDCCKSCGCKEKAANDKPIDTCAKDGTRVASNDTVKSCDGGEGYCYDQT 75

QY 243 PAVNDELAYGFAAASAGNEAGWCCGCGCYELTFTSGAASGKKMVMVQVNTTGGDLGSHF 302
Db 76 PWQVSDSLSYGFAAAACCG-GESGACCCYELTFTSGVPNGKMMVQVNTTGGDLGSHF 134

QY 303 DLOMPGGVGIFNGCAAGWAPNDGARGYGVSSVSDCASLPSALQAGCKWRNWFKN 362
Db 135 DLAIPEGVGVIYNGCTQSGAPSDGWSRYGVSSRSECSQLPSGLQAGCQWRFDWFQNA 194

QY 363 DNPTMTFKEVTCPAELTTRSGCER 386
Db 196 DNPSINFNQVTCPSLTIARTNCKR 218

RESULT 5
QYH87          PRELIMINARY;      PRT;      219 AA.
ID QYH87
AC QYH87;
DT 01-OCT-2000 (TremBLrel. 15, Created)
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SQ SEQUENCE 219 AA; 23126 MW; A712EF3F3CAB041C CRC64;

Query Match      37.2%; Score 783.5; DB 14; Length 219;
Best Local Similarity 66.2%; Pred. No. 1.2e-42;
Matches 135; Conservative 31; Mismatches 35; Indels 3; Gaps 2;

QY 185 SGSTRYWDCCKASCWPVKASVTGPVDTCASNGISLLDAN--AOSGCGNGGFMCMNNQ 242
Db 16 SGRTRYWDCCKASCWEKAAVTQPVDTCAKDGTRVASNDTVKSCDGGEGYCYDQA 75

QY 243 PAVNDELAYGFAAASAGNEAGWCCGCGCYELTFTSGAASGKKMVMVQVNTTGGDLGSHF 302
Db 76 PAVNDSVAYGFAAAACCG-GESGACCCYELTFTSGVPNGKMMVQVNTTGGDLGSHF 134

QY 303 DLOMPGGVGIFNGCAAGWAPNDGARGYGVSSVSDCASLPSALQAGCKWRNWFKN 362
Db 135 DLAIPEGVGVIYNGCTQSGAPSDGWSRYGVSSRSECSQLPSGLQAGCQWRFDWFQNA 194

QY 363 DNPTMTFKEVTCPAELTTRSGCER 386
Db 196 DNPSINFNQVTCPSLTIARTNCKR 218

RESULT 4
QYH89          PRELIMINARY;      PRT;      219 AA.
ID QYH89
AC QYH89;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TremBLrel. 20, Last annotation update)
DE Family 45 cellulase homologue.
OS unclassified eukaryotes.
OC Eukaryota.
OX NCBI_TaxID=42452;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
RL protists in the hindgut of termite Reticulitermes speratus.";
DR EMBL; AB045174; BAA98044.1; -
DR HSSP; P43316; 2ENG.
DR InterPro; IPR000334; GH_45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.
SQ SEQUENCE 219 AA; 23033 MW; CA295CAD8F393199 CRC64;

Query Match      37.1%; Score 780.5; DB 14; Length 219;
Best Local Similarity 64.2%; Pred. No. 1.9e-42;
Matches 131; Conservative 33; Mismatches 37; Indels 3; Gaps 2;

QY 185 SGSTRYWDCCKASCWPVKASVTGPVDTCASNGISLLDAN--AOSGCGNGGFMCMNNQ 242
Db 16 SGRTRYWDCCKSCGCKEKAANDKPIDTCAKDGTRVASNDTVKSCDGGEGYCYDQT 75

QY 243 PAVNDELAYGFAAASAGNEAGWCCGCGCYELTFTSGAASGKKMVMVQVNTTGGDLGSHF 302
Db 76 PWQVSDSLSYGFAAAACCG-GESGACCCYELTFTSGVPNGKMMVQVNTTGGDLGSHF 134

QY 303 DLOMPGGVGIFNGCAAGWAPNDGARGYGVSSVSDCASLPSALQAGCKWRNWFKN 362
Db 135 DLAIPEGVGVIYNGCTQSGAPSDGWSRYGVSSRSECSQLPSGLQAGCQWRFDWFQNA 194

QY 363 DNPTMTFKEVTCPAELTTRSGCER 386
Db 196 DNPSINFNQVTCPSLTIARTNCKR 218

RESULT 5
QYH87          PRELIMINARY;      PRT;      219 AA.
ID QYH87
AC QYH87;
DT 01-OCT-2000 (TremBLrel. 15, Created)
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RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB045167; BAA98037.1; -
 DR EMBL; AB045166; BAA98036.1; -
 DR HSP; P43316; 2ENG.
 DR InterPro; IPR000334; GH_45.
 DR Pfam; PF02015; Glyco_hydro_45; 1.
 DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.
 SQ SEQUENCE 220 AA; 23108 MW; 97738D831BCFASF3 CRC64;

Query Match 36.4%; Score 766.5; DB 14; Length 220;

Best Local Similarity 64.2%; Pred. No. 1.5e-41;
 Matches 131; Conservative 29; Mismatches 41; Indels 3; Gaps 2;

QY 185 SGSTTRYWDCCKKASCSWPKASVTGPVDTCSANGISLLDAN--AQSGCNGGNGFMCNNQ 242

DB 17 SGKTRTRYWDCCKKSGWEAKADVSKPIDTCAKGTTRVASNDTVKSGCDGGGYMCYDQT 76

QY 243 PVAVNDELAYGFAAASIAAGSNEAGWCCGCGCYELTFTSGAAGKMWVQVNTGGDLGSHF 302

DB 77 PWGVNDSYALGFAAASIAAGSNEAGWCCGCGCYELTFTSGAAGKMWVQVNTGGDLGSHF 135

QY 303 DLQMPGGVGIFNGCAAGWAPNDGWARYGGVSSVSDCASLPALQAGCKWRNFWKNS 362

DB 136 DLAIPEGGGVGIYNGCTAQSGAPADGWGSGRYGGVSSRSECSQLPSGLQAGCQWRFDWFQNA 195

QY 363 DNPMTTFKEVTCPAELTTRSGCER 386

DB 196 DNPINFNWVSCPSBELIAKTNCRR 219

RESULT 9

QYJH86 PRELIMINARY; PRT; 219 AA.

ID QYJH86

AC QYJH86

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE Family 45 cellulase homologue.

OS unclassified eukaryotes.

OC Eukaryota.

OX NCBI_TaxID=42452;

RN [1]

RP SEQUENCE FROM N.A.

RA Ohtoko K., Okuma M., Moriya S., Kudo T.;

RT "Diverse genes of family 45 cellulase homologues of the symbiotic

protists in the hindgut of termite Reticulitermes speratus.";

RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB045177; BAA98047.1; -

DR HSP; P43316; 2ENG.

DR InterPro; IPR000334; GH_45.

DR Pfam; PF02015; Glyco_hydro_45; 1.

DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.

SQ SEQUENCE 219 AA; 23158 MW; ECD686EAB8ED1DDI CRC64;

Query Match 36.3%; Score 764.5; DB 14; Length 219;

Best Local Similarity 62.7%; Pred. No. 2e-41;
 Matches 128; Conservative 32; Mismatches 41; Indels 3; Gaps 2;

QY 185 SGSTTRYWDCCKKASCSWPKASVTGPVDTCSANGISLLDAN--AQSGCNGGNGFMCNNQ 242

DB 16 SGKTRTRYWDCCKKSGWEAKADVSKPIDTCAKGTTRVASNDTVKSGCDGGGYMCYDQT 75

QY 243 PVAVNDELAYGFAAASIAAGSNEAGWCCGCGCYELTFTSGAAGKMWVQVNTGGDLGSHF 302

DB 76 PMSVNDYSYGPAAACCG-GESGACCGCYDLTFTSGVPNGKMTVQITNTGGDLGSHF 134

QY 303 DLQMPGGVGIFNGCAAGWAPNDGWARYGGVSSVSDCASLPALQAGCKWRNFWKNS 362

DB 135 DLAIPEGGGVGIYNGCTAQSGAPADGWGSGRYGGVSSRSECSQLPSGLQAGCQWRFDWFQNA 194

QY 363 DNPMTTFKEVTCPAELTTRSGCER 386

DB 195 DNPINFNWVSCPSBELIAKTNCRR 218

RESULT 10

QYJH94 PRELIMINARY; PRT; 221 AA.

ID QYJH94

AC QYJH94

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE Family 45 cellulase homologue.

OS unclassified eukaryotes.

OC Eukaryota.

OX NCBI_TaxID=42452;

RN [1]

RP SEQUENCE FROM N.A.

RA Ohtoko K., Okuma M., Moriya S., Kudo T.;

RT "Diverse genes of family 45 cellulase homologues of the symbiotic

protists in the hindgut of termite Reticulitermes speratus.";

RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB045169; BAA98039.1; -

DR HSP; P43316; 2ENG.

DR InterPro; IPR000334; GH_45.

DR Pfam; PF02015; Glyco_hydro_45; 1.

DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.

SQ SEQUENCE 221 AA; 23220 MW; 8A84CEB0A8C46372 CRC64;

Query Match 36.2%; Score 762.5; DB 14; Length 221;

Best Local Similarity 63.2%; Pred. No. 2.7e-41;
 Matches 129; Conservative 34; Mismatches 38; Indels 3; Gaps 2;

QY 185 SGSTTRYWDCCKKASCSWPKASVTGPVDTCSANGISLLDAN--AQSGCNGGNGFMCNNQ 242

DB 17 SGKTRTRYWDCCKKSGWEAKADVSKPIDTCAKGTTRVASNDTVKSGCDGGGYMCYDQT 76

QY 243 PVAVNDELAYGFAAASIAAGSNEAGWCCGCGCYELTFTSGAAGKMWVQVNTGGDLGSHF 302

DB 77 PVAVNDYSYLGFAAASIAAGSNEAGWCCGCGCYELTFTSGVPNGKMTVQITNTGGDLGSHF 135

QY 303 DLQMPGGVGIFNGCAAGWAPNDGWARYGGVSSVSDCASLPALQAGCKWRNFWKNS 362

DB 136 DLAIPEGGGVGIYNGCTAQSGAPADGWGSGRYGGVSSRSECSQLPSGLQAGCQWRFDWFQNA 195

QY 363 DNPMTTFKEVTCPAELTTRSGCER 386

DB 196 DNPINFNWVSCPSBELIAKTNCRR 219

RESULT 11

QYJH88 PRELIMINARY; PRT; 219 AA.

ID QYJH88

AC QYJH88

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE Family 45 cellulase homologue.

OS unclassified eukaryotes.

OC Eukaryota.

OX NCBI_TaxID=42452;

RN [1]

RP SEQUENCE FROM N.A.

RA Ohtoko K., Okuma M., Moriya S., Kudo T.;

RT "Diverse genes of family 45 cellulase homologues of the symbiotic

protists in the hindgut of termite Reticulitermes speratus.";

RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB045175; BAA98045.1; -

DR HSP; P43316; 2ENG.

DR InterPro; IPR000334; GH_45.

DR Pfam; PF02015; Glyco_hydro_45; 1.

DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.

SQ SEQUENCE 219 AA; 23030 MW; 179BF1344C6D7024 CRC64;

Query Match 36.1%; Score 759.5; DB 14; Length 219;

Best Local Similarity 62.7%; Pred. No. 4.1e-41;

Db 136 DLAIPEGGVGYNGTAGAPADGWSKYGVSRSRSCSQLPSGLQAGCQWRFDWFOA 195
Qy 363 DNPWTMTFKVTCPAELTTRSGCER 386
Db 196 DNPSINFNVVSCPGELIANTNCRR 219

RESULT 15

O93782 PRELIMINARY; PRT; 305 AA.
AC O93782;
DT 01-MAY-1999 (TRENBLrel. 10, Created)
DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Endoglucanase.
GN EGL3.
OS Humicola grisea var. thermoidea.
OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola.
OX NCBI_TaxID=5528;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO9854;
RX MEDLINE=99144540; PubMed=990729;
RA Takashima S., Iikura H., Nakamura A., Hidaka M., Masaki H., Uozumi T.;
RT "Comparison of gene structures and enzymatic properties between two
RT endoglucanases from Humicola grisea";
RL J. Biotechnol. 67:85-97(1999).
DR EMBL; AB003107; BAA74956.1; -.
DR HSP; P43316; 2ENG.
DR InterPro; IPR000254; CBD fungal.
DR InterPro; IPR000334; GH_45.
DR Pfam; PF00734; CEM 1; 1.
DR ProDom; PD001821; Glyco hydro 45; 1.
DR SMART; SM00236; fCBD_1.
DR PROSITE; PS00562; CBD_FUNGAL; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; 1.
SQ SEQUENCE 305 AA; 32174 MW; 28C979D6EDCD771D CRC64;

Query Match 34.1%; Score 718; DB 3; Length 305;
Best Local Similarity 61.7%; Pred. No. 2.5e-38;
Matches 127; Conservative 26; Mismatches 47; Indels 6; Gaps 3;
Qy 183 SGSGSTTRYWDCCKASCSWPGKASVTGPVDTCASNGISLLDANAQGCN-GGNGFMCNNN 241
Db 21 AADGKSTRYWDCCPKSCGWAKAPVNPVFCNANFQRLTDFDAKSGCEPGGVAYSCADQ 80
Qy 242 QPWAYNDELAVGFAAASIAGSNEAGWCCGYELTFTSGAASGKKMNVQVNTTGGDLGSNH 301
Db 81 TFWAYNDFFAFGFAATSAGSNEAGWCCACVYELTFTSGFVAGKKMNVQVSTSTGGDLGSNH 140
Qy 302 FDLQPGGGVGIFNGCAAWGA-PNDGNGARYGGVSSVSDCASLPALQAGCKWRFNWFK 360
Db 141 FDLNIPGGGVGIFDGCCTQFGGLP----GQRYGGISSRNECDRFPDALKPGCYWRFDWFK 196
Qy 361 NSDNPMTFTKVTCPAELTTRSGCER 386
Db 197 NADNPSFSFRVQCPAELVARTGCR 222

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